This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1.   **(Currently Amended)**   A method of determining a phenotype of a retrovirus, wherein the retrovirus is the Human Immunodeficiency Virus, comprising:

a)   obtaining from a patient a sample comprising at least one of a plasma sample, a blood sample, a saliva sample, mucous sample, and a tissue sample;

[[a)]]b)   obtaining a genetic sequence of the Human Immunodeficiency Virus;

[[b)]]c)   identifying a mutation pattern of the genetic sequence of the Human Immunodeficiency Virus, wherein said mutation pattern comprises at least one mutation that correlates to resistance to at least one therapy;

[[c)]]d)   searching a relational genotype/phenotype database for at least one database mutation pattern similar to said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus;

[[d)]]e)   obtaining at least one database phenotype of the at least one database mutation pattern; and

[[e)]]f)   determining the phenotype of the Human Immunodeficiency Virus from the at least one database phenotype.

2.   **(Original)**   The method of claim 1, wherein a series of phenotypes is obtained by repeating steps b) through e) for each therapy in a group of therapies.

3.   **(Previously Presented)**   The method of claim 1, wherein said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus is specific to a therapy.

4-7.   **(Canceled)**

8.   **(Previously Presented)**   The method of claim 1, wherein said at least one mutation is chosen from a frame shift mutation, a base substitution, and an epigenetic mutation.

9-12.   **(Canceled)**

13.   **(Previously Presented)**   The method of claim 1, wherein the genetic sequence of Human Immunodeficiency Virus is the genetic sequence of the protease region of the Human Immunodeficiency Virus genome, the genetic sequence of the reverse transcriptase region of the Human Immunodeficiency Virus genome, or the genetic sequence of the protease region and reverse transcriptase region of the Human Immunodeficiency Virus genome.

14-15. **(Canceled)**

16.   **(Previously Presented)**   The method of claim 1, wherein said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus comprises at least two mutations that correlate to resistance to at least one therapy.

17.   **(Original)**   The method of claim 1, wherein the search of the relational genotype/phenotype database for at least one sample with a similar mutation pattern uses cluster searches.

18.   **(Previously Presented)**   The method of claim 1, wherein the database mutation pattern comprises at least one mutation found in said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus.

19.   **(Previously Presented)**   The method of claim 1, wherein the database mutation pattern is a mutation pattern in which at least about 50% of the mutations are identical to said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus.

20.   **(Previously Presented)**   The method of claim 19, wherein the database mutation pattern is a mutation pattern in which at least about 80% of the mutations are identical to said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus.

21.   **(Previously Presented)**   The method of claim 20, wherein the database mutation pattern is a mutation pattern in which at least about 90% of the mutations are identical to said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus.

22.   **(Previously Presented)**   The method of claim 21, wherein the mutations of the database mutation pattern are identical to said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus.

23.   **(Previously Presented)**   The method of claim 1, wherein the phenotype of the Human Immunodeficiency Virus is a mean fold-change in resistance, wherein said mean fold change is obtained from all of the database phenotypes obtained in step d).

24.   **(Previously Presented)**   The method of claim 1, wherein the phenotype of the Human Immunodeficiency Virus is expressed as an IC_{50}.

25.   **(Previously Presented)**   A method of reporting a phenotype for a Human Immunodeficiency Virus, comprising generating a report having the phenotype determined using the method of claim 1.

26-27. **(Canceled)**

28.   **(Currently amended)**   A method of determining a phenotype of a retrovirus, wherein the retrovirus is the Human Immunodeficiency Virus comprising:

a).   obtaining from a patient a sample comprising at least one of a plasma sample, a blood sample, a saliva sample, mucous sample, and a tissue sample;

[[a)]]b)   obtaining a genetic sequence of the Human Immunodeficiency Virus;

[[b)]]c)   searching a relational genotype/phenotype database for at least one database genetic sequence similar to said genetic sequence of the Human Immunodeficiency Virus;

[[c)]]d)   obtaining a database phenotype of the at least one database genetic sequence; and

[[d)]]e)   determining the phenotype of the Human Immunodeficiency Virus from the database phenotype.

29.   **(Previously Presented)**   The method of claim 28, wherein the at least one database genetic sequence is at least about 60% identical to the genetic sequence of the Human Immunodeficiency Virus.

30.   **(Previously Presented)**   The method of claim 29, wherein the at least one database genetic sequence is at least about 70% identical to the genetic sequence of the Human Immunodeficiency Virus.

31.   **(Previously Presented)**   The method of claim 30, wherein the at least one database genetic sequence is at least about 80% identical to the genetic sequence of the Human Immunodeficiency Virus.

32.   **(Previously Presented)**   The method of claim 31, wherein the at least one database genetic sequence is at least about 90% identical to the genetic sequence of the Human Immunodeficiency Virus.

33-38. **(Canceled)**

39.   **(Previously Presented)**   A computer program for determining a phenotype of a retrovirus, wherein the retrovirus is the Human Immunodeficiency Virus, wherein the program is comprised on a computer readable medium, comprising:

a) receiving a genetic sequence from the Human Immunodeficiency Virus from a patient;

b) identifying a mutation pattern of the genetic sequence of the Human Immunodeficiency Virus, wherein said mutation pattern comprises at least one mutation that correlates to resistance to at least one therapy;

c) searching a relational genotype/phenotype database for at least one database mutation pattern similar to said mutation pattern of the genetic sequence of the Human Immunodeficiency Virus;

d) obtaining at least one database phenotype of the at least one database mutation pattern from the relational genotype/phenotype database;

e) determining the at least one phenotype of Human Immunodeficiency Virus from the at least one database phenotype; and

f) providing the phenotype of the Human Immunodeficiency Virus sample.

40.   **(Original)**   The computer program of claim 39, wherein a series of phenotypes is obtained by repeating steps b) through e) for a group of therapies.

41.   **(Previously Presented)**   The computer program of claim 40, wherein the phenotype of the Human Immunodeficiency Virus is provided in a report.

42.   **(Canceled)**